

Supplementary Materials

Combining Transcriptome- and Metabolome-Analyzed Differentially Expressed Genes and Differential Metabolites in Development Period of *Caoyuanheimo-1* (*Agaricus* sp.) from Inner Mongolia, China

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1 Supplementary Data

Figure S1. Metabolome PCA analysis of HY and HZ(a), HY and HC(b), HZ and HC(c).

Figure S2. Statistics of transcripts and unigenes in transcriptome data.

Figure S3. Transcriptome PCA analysis of HY, HZ and HC.

Figure S4. Differentially expressed genes(DEGs) KEGG enrichment analysis of HY vs HC.

Figure S5. Differentially expressed genes(DEGs) KEGG enrichment analysis of HZ vs HC.

Figure S6. Differentially expressed genes(DEGs) KEGG enrichment analysis of HY vs HZ.

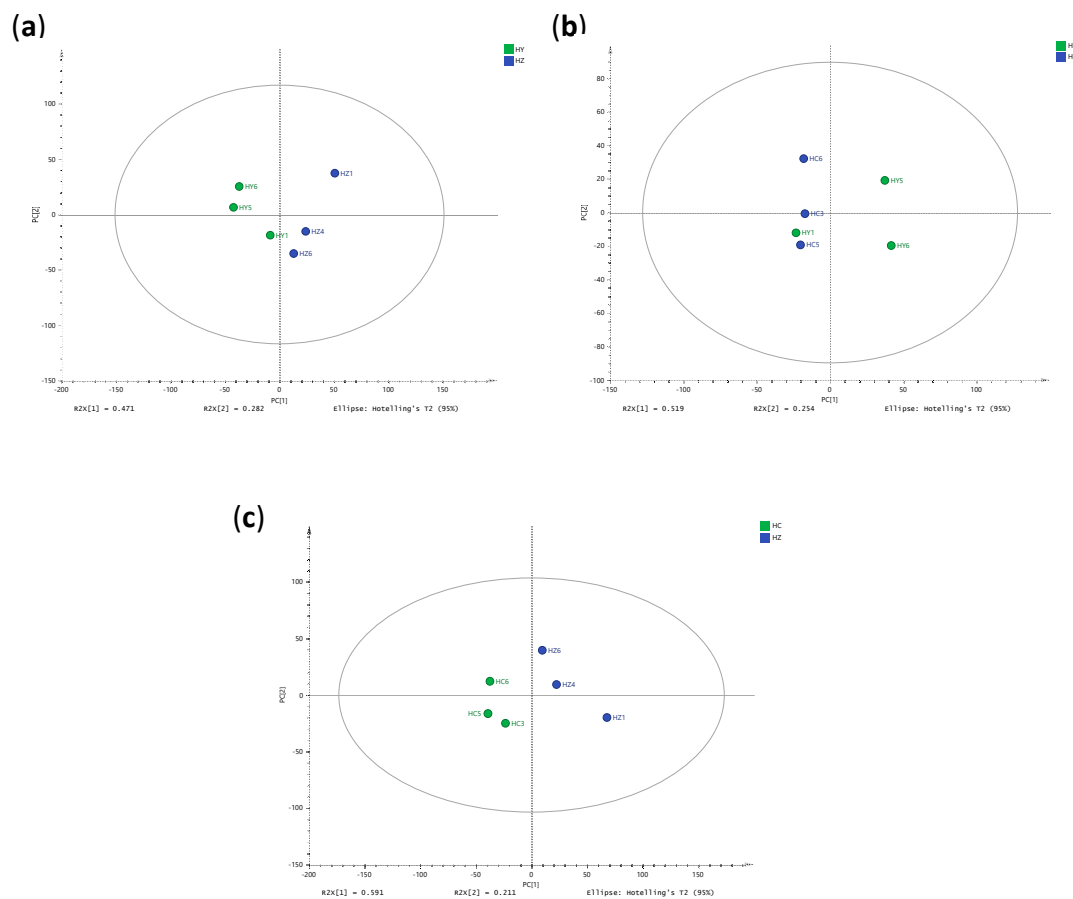


Figure S1. Metabolome PCA analysis of HY and HZ(a),HY and HC(b),HZ and HC(c).

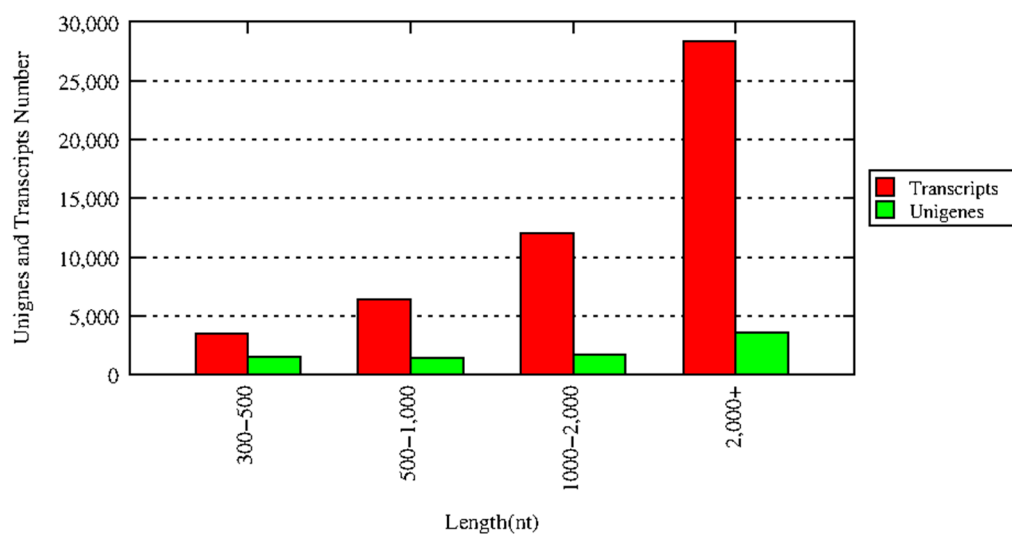


Figure S2. Statistics of transcripts and unigenes in transcriptome data. The X-axis represents different length intervals of Unigene; The Y-axis represents the number and proportion of Unigenes within a certain length range.

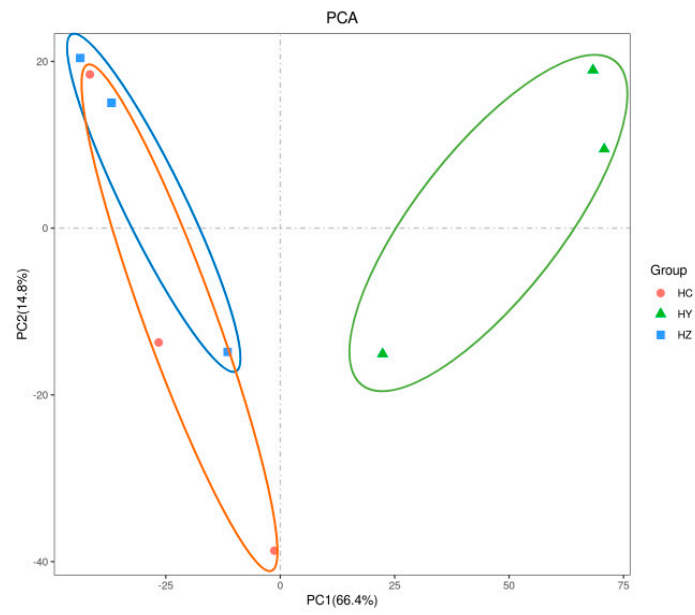


Figure S3. Transcriptome PCA analysis of HY, HZ and HC.

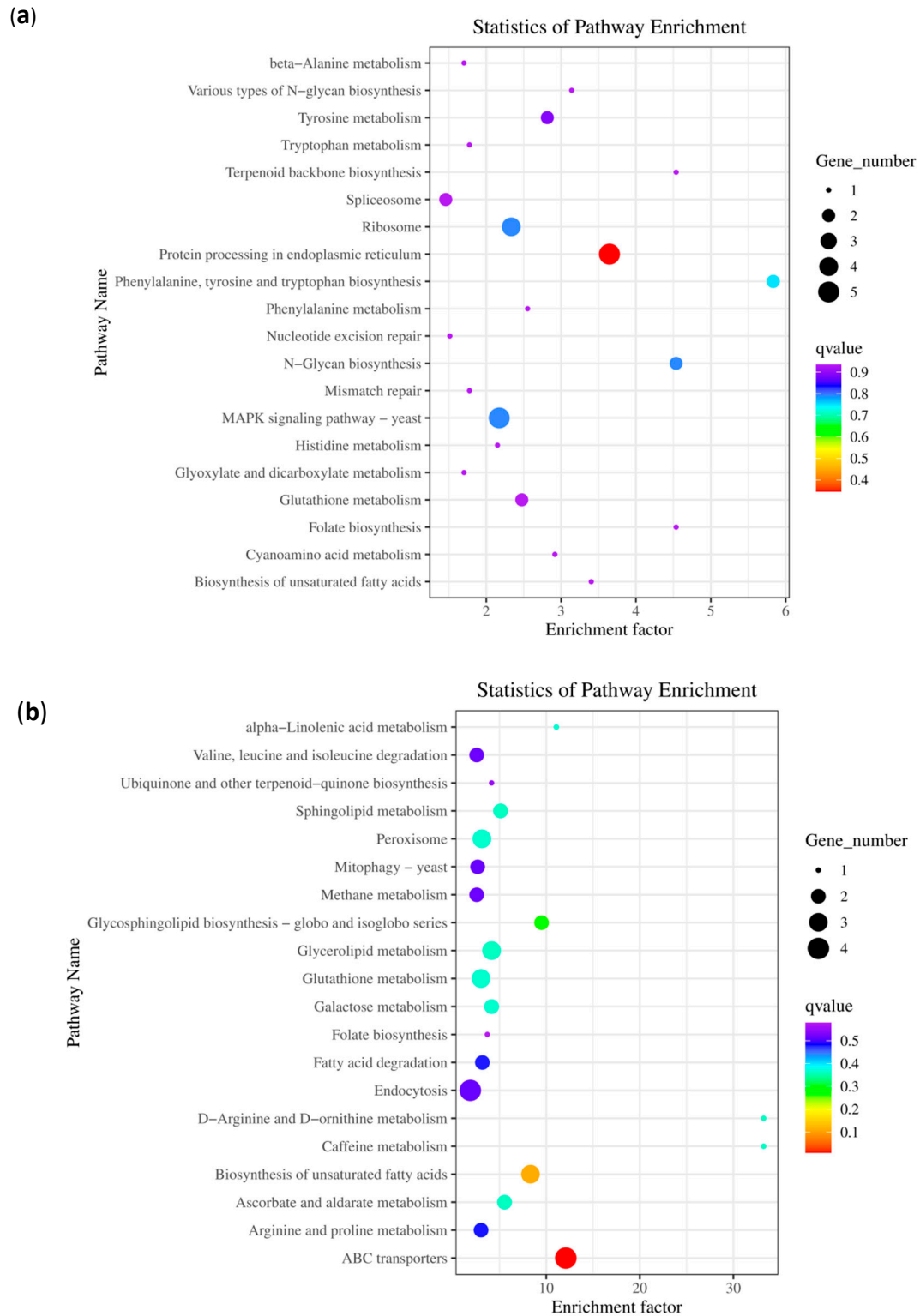


Figure S4. Differentially expressed genes(DEGs) KEGG enrichment analysis of HY vs HC. **(a)** The genes upregulated in HC in the HY vs HC group. **(b)** The genes downregulated in HC in the HY vs HC group.

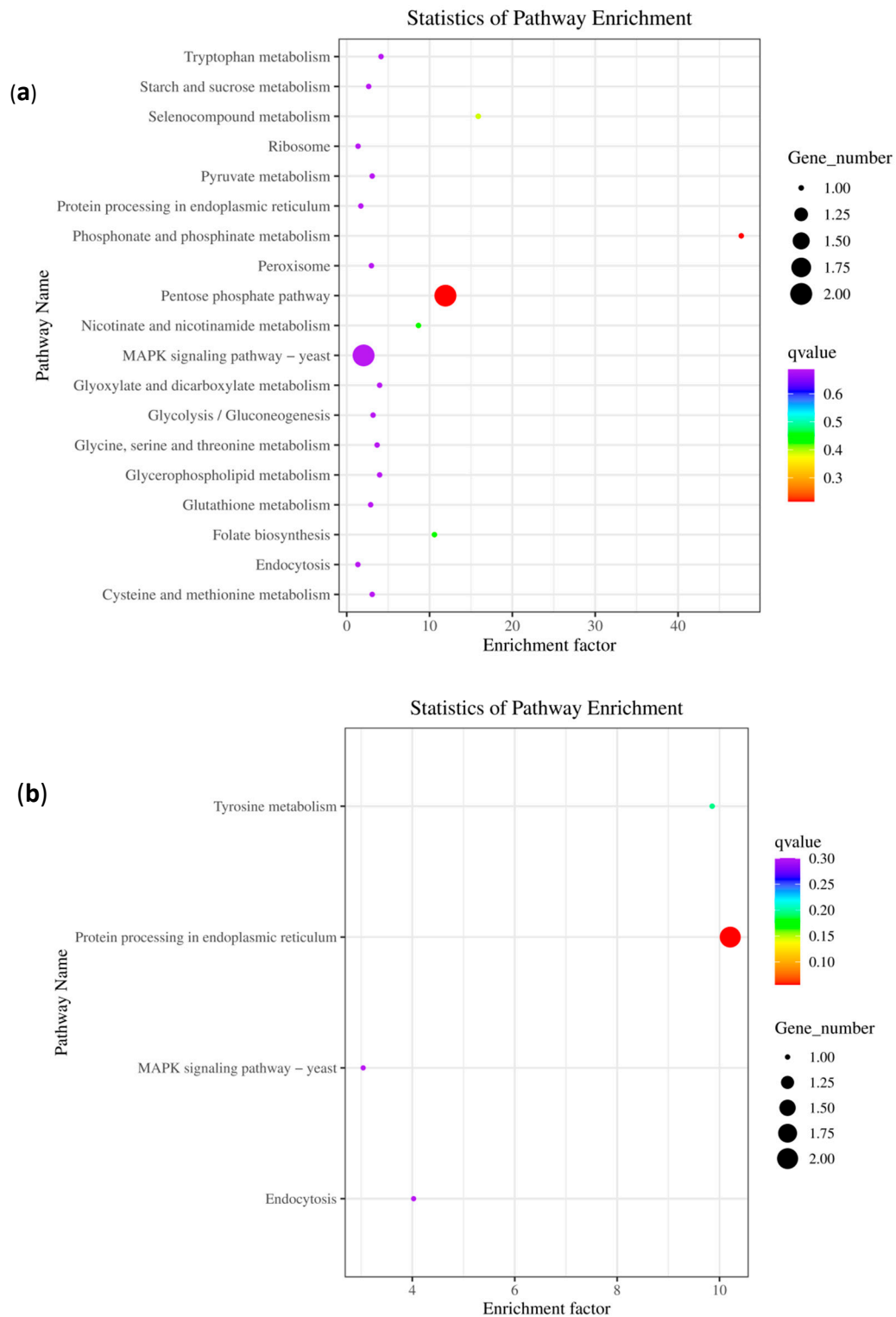


Figure S5. Differentially expressed genes(DEGs) KEGG enrichment analysis of HZ vs HC. **(a)** The genes upregulated in HC in the HZ vs HC group. **(b)** The genes downregulated in HC in the HZ vs HC group.

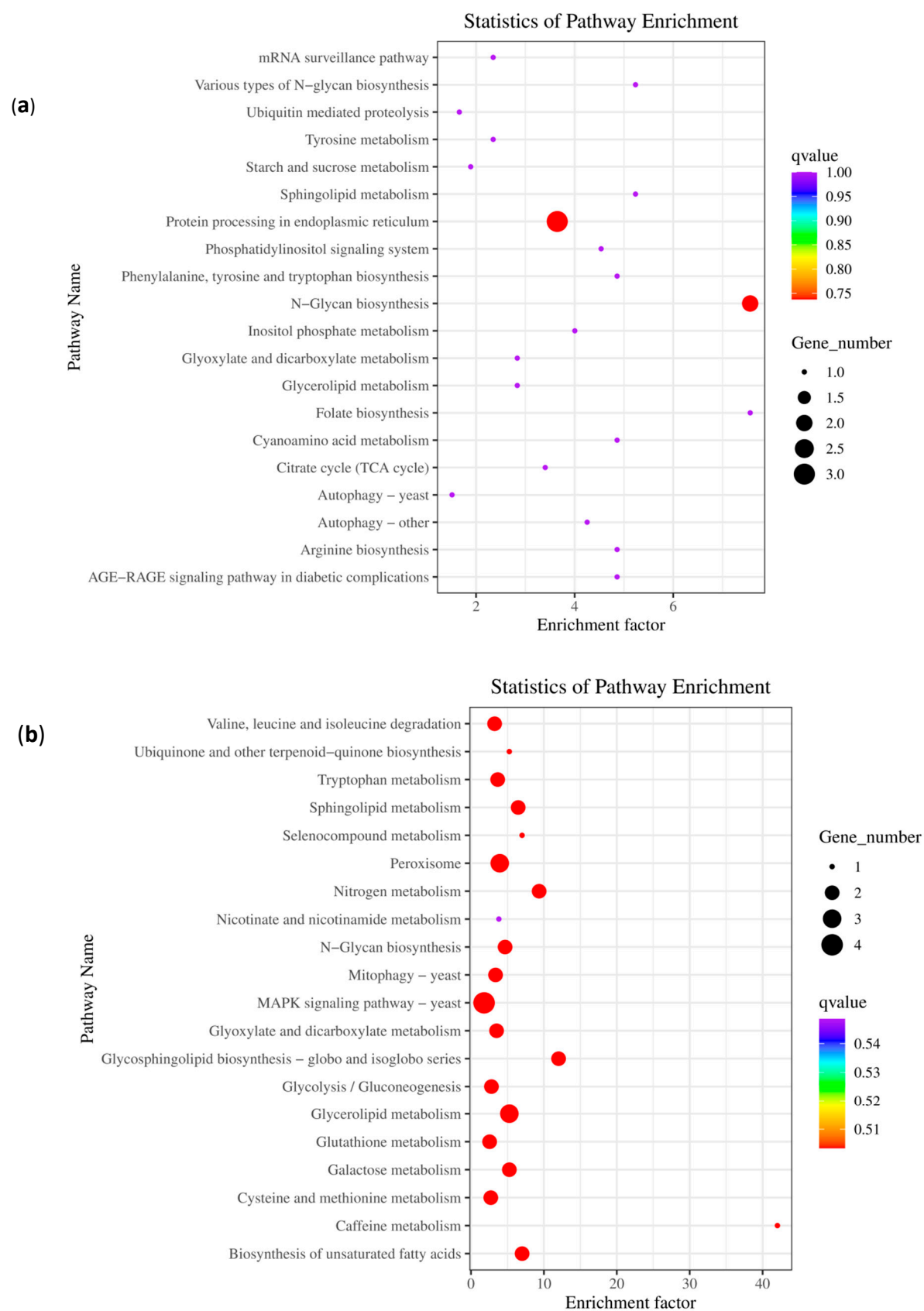


Figure S6. Differentially expressed genes(DEGs) KEGG enrichment analysis of HY vs HZ. **(a)** The genes upregulated in HZ in the HY vs HZ group. **(b)** The genes downregulated in HZ in the HY vs HZ group.

